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HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
530 VIRGINIA ROAD
P.O. BOX 9133
CONCORD, MA 01742-9133

EXAMINER	
LONG, SCOTT	

ART UNIT	PAPER NUMBER
1633	

DATE MAILED: 09/19/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/783,994	REINHERZ ET AL.	
	Examiner	Art Unit	
	Scott D. Long	1633	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *13 July 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-38* is/are pending in the application.

4a) Of the above claim(s) *9 and 13-38* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) *1-8 and 10-12* is/are rejected.

7)☐ Claim(s) *1* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *20 February 2004 and 30 July 2004* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *10/31/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Examiner acknowledges the election, without traverse, of Group I directed to isolated DNA SEQ ID NO:1, fragments thereof, and associated plasmids, vectors, probes, in the reply filed on 8 June 2006.

Claim Status

Claims 1-38 are pending. However, claims 9 and 13-38 are withdrawn from further consideration by the Examiner, pursuant to 37 CFR 1.142(b), as being drawn to non-elected inventions, there being no allowable generic or linking claim. Claims 1-8 and 10-12 are under current examination.

Sequence Compliance

Sequence Listing and CRF have been received and are acknowledged by examiner. A statement that the Computer Readable Form (CRF) and the Sequence Listing are identical has been submitted and is acknowledged by examiner.

Figure 2 is not sequence compliant. There are sequences within Figure 2 that are not identified using required format, e.g. "SEQ ID NO:1."

Information Disclosure Statement

The Information Disclosure Statements (IDS) filed on 20 February 2006 consisting of 1 sheet is in compliance with 37 CFR 1.97. Accordingly, examiner has considered the Information Disclosure Statements.

Priority

This application claims benefit from PCT/US02/08288 (filed 14 March 2002) which claims benefit from provisional US Application 60/314,046 (filed 21 Aug 2001) and from provisional US Application 60/322,993 (filed 18 Sept 2001). The instant application has been granted the benefit date, 18 September 2001, from the application 60/322,993.

Drawings

Color photographs and color drawings are not accepted unless a petition filed under 37 CFR 1.84(a)(2) is granted. Any such petition must be accompanied by the appropriate fee set forth in 37 CFR 1.17(h), three sets of color drawings or color photographs, as appropriate, and, unless already present, an amendment to include the following language as the first paragraph of the brief description of the drawings section of the specification:

> The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

Color photographs will be accepted if the conditions for accepting color drawings and black and white photographs have been satisfied. See 37 CFR 1.84(b)(2).

Claim Objections

Claim 1 is objected to as encompassing non-elected invention. Claim language should be amended to read on only elected species/group invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

WRITTEN DESCRIPTION

Claim 7 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The methodology for determining adequacy of Written Description to convey that applicant was in possession of the claimed invention includes determining whether the application describes an actual reduction to practice, determining whether the invention is complete as evidenced by drawings or determining whether the invention has been set forth in terms of distinguishing identifying characteristics as evidenced by other descriptions of the invention that are sufficiently detailed to show that applicant was in

possession of the claimed invention (*Guidelines for Examination of Patent Applications under 35 USC § 112, p 1 "Written Description" Requirement;* (Federal Register/Vol 66. No. 4, Friday, January 5, 2001; II Methodology for Determining Adequacy of Written Description (3.)).

Claim 7 is broadly drawn, such that it applies to any a genus of nucleic acid that hybridizes under high stringency to SEQ ID NO:1. However, the working examples provided in the instant application only demonstrate unspecified (by SEQ ID NO) random-primed labeled IkBNS nucleic acids that hybridize in Northern Blot analysis.

The Revised Interim Guideline for Examination of Patent Applications under 35 USC § 112, p1 "Written Description" Requirement (Federal Register/ Vol 66. No 4, Friday January 5, 2001) states "THE CLAIMED INVENTION AS A WHOLE MAY NOT BE ADEQUATELY DESCRIBED IF THE CLAIMS REQUIRE AN ESSENTIAL OR CRITICAL ELEMENT WHICH IS NOT ADEQUATELY DESCRIBED IN THE SPECIFICATION AND WHICH IS NOT CONVENTIONAL IN THE ART" (column 3, page 71434), "WHEN THERE IS SUBSTANTIAL VARIATION WITHIN THE GENUS, ONE MUST DESCRIBE A SUFFICIENT VARIETY OF SPECIES TO REFLECT THE VARIATION WITHIN THE GENUS", "IN AN UNPREDICTABLE ART, ADEQUATE WRITTEN DESCRIPTION OF A GENUS WHICH EMBRACES WIDELY VARIANT SPECIES CANNOT BE ACHIEVED BY DISCLOSING ONLY ONE SPECIES WITHIN THE GENUS" (column 2, page 71436, emphasis added).

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states that "APPLICANT MUST CONVEY WITH REASONABLE CLARITY TO THOSE SKILLED IN THE ART THAT, AS OF THE FILING DATE SOUGHT, HE OR SHE WAS IN POSSESSION OF THE INVENTION. THE INVENTION IS, FOR PURPOSES OF THE 'WRITTEN DESCRIPTION' INQUIRY, *WHATEVER IS NOW CLAIMED.*" (See page

1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize the [he or she] invented what is claimed." (See *Vas-Cath* at page 1116).

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481, 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

With respect to claims limiting a polynucleotide by hybridization conditions, even under relatively high stringent conditions, the claimed nucleotide sequence could hybridize to a genus of polynucleotides that are similar, but not identical to the recited polynucleotides. The limitation by hybridization is obviously generic to a considerable number of nucleotides varying in the length of the nucleic acids, the degree of homologies among the sequences, and the biological activities of the encoded polypeptides, which may or may not be involved in the function of IkBNS. This genus also embraces sub-sequences that are unknown and include unsequenced polynucleotides, whose function is yet to be determined.

Considering the potentially large numbers of polynucleotides encompassed by these claims, the disclosure is not sufficient to show that a skilled artisan would recognize that the applicant was in possession of the claimed invention (genus) commensurate to its scope at the time the application was filed.

ENABLEMENT

Claims 7 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The factors to be considered in determining whether undue experimentation is required are summarized *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988). The Court in *Wands* states: "Enablement is not precluded by the necessity for some 'experimentation.'" Clearly, enablement of a claimed invention cannot be predicated on the basis of quantity of experimentation required to make or use the invention. "Whether undue experimentation is needed is not a single simple factual determination, but rather is a conclusion reached by weighing many factual considerations." (*Wands*, 8 USPQ2d 1404). The factors to be considered in determining whether undue experimentation is required include: (1) the quantity of experimentation necessary, (2) the amount or direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. While all of these factors are considered, a sufficient amount for a prima facie case is discussed below.

Nature of the Invention

The full scope of the claimed invention encompasses an enormous number of nucleic acids which could hybridize with SEQ ID NO:1, the complement of SEQ ID

NO:1, a portion of SEQ ID NO:1 which is at least 500 nucleotides in length, or a nucleic acid sequence that encodes SEQ ID NO:2. The size of these hybridizing nucleic acids might be small, or equal in size to full-length SEQ ID NO:1, or larger than SEQ ID NO:1. The nucleic acids might also encompass very large nucleic acids that hybridize under highly stringent conditions only over a short range near one end of both sequences. In this case, there would be a very low level of homology between the two sequences, despite high stringency hybridization.

With respect to claims limiting a polynucleotide by hybridization conditions, even under relatively high stringent conditions, the claimed nucleotide sequence could hybridize to a genus of polynucleotides that are similar, but not identical to the recited polynucleotides. The limitation by hybridization is obviously generic to a considerable number of nucleotides varying in the length of the nucleic acids, the degree of homologies among the sequences, and the biological activities of the encoded polypeptides, which may or may not be involved in the function of IkBNS. This genus also embraces sub-sequences that are unknown and include unsequenced polynucleotides, whose function is yet to be determined.

Working Examples and Guidance Provided

The instant application suggests that hybridizing nucleic acids might be "greater than about 75 percent, more preferably greater than about 80 percent, and even more preferably greater than about 90 percent, identical to a nucleotide sequence...consisting of SEQ ID NO:1" (Spec., page 3, lines 27-29). Other than these preferred homologies,

there is no guidance given for nucleic acids that meet the limitations of Claim 7, but are not probes as in Claim 8. Neither are there working examples of nucleic acids that have been isolated through the stringent hybridization method. Furthermore, there are no examples of nucleic acid sequences described in the specification that conform to the limitations of claim 7.

State of the Art and Analysis of the Issues

A skilled artisan would not know how to make a nucleic acid which corresponds to the large number of species of nucleic acid encompassed by Claim 7. Some of the nucleic acids that fit within the genus of Claim 7 would not be homologues of SEQ ID NO:1. In fact, despite hybridizing under high stringency conditions, these molecules would be structurally and functionally unrelated to SEQ ID NO:1-2. Sequences which fit into this class of unrelated molecules would require further research in order for an artisan to learn how to use them. Furthermore, the artisan would have no reason to make such sequences.

Walcott (CLINICAL MICROBIOLOGY REVIEWS, Oct. 1992, p. 370-386) teaches "hybridization...is subject to...nonspecific background interference" (page 372, column 1) and "hybridization studies...produced...false-positive reactions" (page 371, column 2). Walcott further teaches "short probes...are subject to more nonspecific hybridizations, are limited in specificity, and are more difficult to label....Long probes hybridize more stably than short probes at high temperatures and low salt

concentrations (low stringency)." (page 371, column 2). Gress et al. (*Mammalian Genome 3:* 609-619, 1992) teach, "complex probes usually generate a high amount of background and unspecific hybridization." (page 610, column 1). The teachings of Walcott and Gress et al. cast doubt on the homology of the sequences derived through hybridization methods. If sequences that hybridize under stringent conditions are not homologous or functionally related to those sequences of the genus of claim 7, then there is surely difficulty for the artisan to make and/or use these sequences. Or if the amount of relatedness of the hybridizing sequence to SEQ ID NO:1 is only comprises a single domain, then the artisan would likewise encounter difficulty in using these sequences and would be required to perform further investigation to find a utility for these discovered sequences.

Therefore, the quantity of experimentation required to make and/or use the invention, as claimed, is insufficient to enable the invention.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-2 and 4-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Lamerdin et al (GenBank Accession No. AD000864. 22 March 1997).

Claim 1 is directed to "an isolated nucleic acid molecule consisting of a nucleic acid sequence selected from...a nucleic acid that encodes SEQ ID NO:2."

The Lamerdin et al. sequence teaches all of the 15000 bases of SEQ ID NO:1. See also FASTA alignment of SEQ ID NO:1 and GenBank Acc# AD000864 for comparison of sequences. The claim language of claim 1 contains closed language ("consisting of") followed by open language ("encodes"). Many molecules can encode SEQ ID NO:2. For example, a cDNA molecule can encode SEQ ID NO:2. However, the instant Specification (page 2, lines 20-27) indicates that SEQ ID NO:1 can encode SEQ ID NO:2. Since SEQ ID NO:1 contains introns and encodes SEQ ID NO:2, the GenBank sequence AD000864 which comprises SEQ ID NO:1 that is capable of encoding SEQ ID NO:2 and therefore meets the limitations of claim 1-i. It should also be noted that the annotations on Figure 9-A that indicate the Exons within the IkBNS genomic sequence do not indicate the start codon or amino acids M and E, which could occur upstream of the indicated exon I, perhaps beginning at base 471 (encodes amino acids Methionine and Glutamic Acid and has donor (GT) splice site).

Claim 2 is directed to the further limitation that the nucleic acid is "DNA." Lamerdin et al. teach a DNA sequence, satisfying the limitation of claim 2.

Claim 4 is directed to "an isolated nucleic acid molecule comprising a nucleic acid sequence selected from...a nucleic acid that encodes SEQ ID NO:2." As described above, Lamerdin et al. sequence, GenBank Accession Number AD000864, comprises SEQ ID NO:1 which comprises a nucleic acid that encodes SEQ ID NO:2.

Claim 5 is directed to the further limitation that the nucleic acid is "DNA." Lamerdin et al. teach a DNA sequence, satisfying the limitation of claim 5.

Accordingly, Lamerdin et al. anticipated the instant claims, 1-2 and 4-5 .

Claim 7 is directed to a nucleic acid that hybridizes under high stringency conditions to SEQ ID NO:1. The Lamerdin et al sequence would hybridize to SEQ ID NO:1 under high stringency conditions.

Claim 7-8 is rejected under 35 U.S.C. 102(b) as being anticipated by Rosen et al. (WO/2000/58468A2). Rosen et al. teach a sequence of named SEQ ID NO:17 in the cited patent (page 7 of Sequence Listing), that has 167 contiguous nucleotides in common with SEQ ID NO:1 of the instant application. This sequence can be used as a probe and could be made to hybridize under high stringency conditions.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein

were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1-3 and 6 are rejected under 35 U.S.C. 103(a) as being anticipated by Lamerdin et al (GenBank Accession No. AD000864. 22 March 1997).

Claim 1 is directed to "an isolated nucleic acid molecule consisting of a nucleic acid sequence selected from a) SEQ ID NO:1; b) the complement of SEQ ID NO:1;...e) a portion of SEQ ID NO:1 which is at least 500 nucleotides in length;...i) a nucleic acid that encodes SEQ ID NO:2." Claim 2 is directed to the further limitation that the nucleic acid is DNA.

The Lamerdin et al. sequence teaches all of the 15000 bases of SEQ ID NO:1, thus GenBank Acc# AD000864 comprises SEQ ID NO:1 and a nucleic acid that encodes SEQ ID NO:2. See also FASTA alignment of SEQ ID NO:1 and GenBank Acc# AD000864 for comparison of sequences. The claim language of claim 1 contains closed language ("consisting of") followed by open language ("encodes"). Many molecules can encode SEQ ID NO:2. For example, a cDNA molecule can encode SEQ ID NO:2. However, the instant Specification (page 2, lines 20-27) indicates that SEQ ID NO:1 can encode SEQ ID NO:2. It should also be noted that the annotations on Figure 9-A that indicate the Exons within the IkBNS genomic sequence do not indicate the start

codon or amino acids M and E, which could occur upstream of the indicated exon I, perhaps beginning at base 471 (encodes amino acids Methionine and Glutamic Acid and has donor (GT) splice site). In addition, the limitation of claim 1-f is met by the sequence of Lamerdin et al., because it contains at least 500 contiguous nucleotides of SEQ ID NO:1.

The Lamerdin et al. sequence teach all of the 15000 bases of SEQ ID NO:1. DNA is intrinsically a double stranded molecule. Any skilled artisan would be able to deduce the complement of a given DNA sequence. In addition, the sequence taught by Lamerdin et al. contains a variety potential sequences that are at least 500 nucleotides. Since no specific rationale is provided in the Specification regarding the reason for at least 500 bases, any subset of the Lamerdin et al. sequence that consists of SEQ ID NO:1 would satisfy this claim limitation.

Claims 3 and 6 are directed to the further limitation that the nucleic acid of claims 1 and 4 are RNA. Any skilled artisan using the sequence taught by Lamerdin et al. would be able to deduce the corresponding RNA of the DNA sequence SEQ ID NO:1 and the RNA that encodes the protein sequence of SEQ ID NO:2.

It would have been obvious to the person of ordinary skill in the art at the time the invention was made to utilize a portion of the sequence of GenBank Acc# AD000864 that contains all of the exons of a gene. The specification of the instant application does not specify why the exact size of 15,000 bases was selected for the invention of SEQ ID NO:1. Therefore, any sequence that contains all of the gene of interest would be equivalent.

The person of ordinary skill in the art would have been motivated to make those modifications because it is a DNA sequence that contains all of the coding sequence of IkBNS.

The skilled artisan would have had a reasonable expectation of success in utilizing the nucleic acid sequence of Lamerdin et al. in place of the nucleic acid sequence of SEQ ID NO:1 or in place of the nucleic acid sequence which encodes SEQ ID NO:2, because the Lamerdin sequence can be substituted for any functions that the sequences of the instant application are put to use.

Therefore the isolated nucleic acid as taught by Lamerdin et al. would have been *prima facie* obvious over the isolated nucleic acid of the instant application.

Claims 10-12 are rejected under 35 U.S.C. 103(a) as being anticipated by Lamerdin et al (GenBank Accession No. AD000864. 22 March 1997) in view of Liu, et al. (Current Biology. 19 November 1998, 8:1300–1309).

Claim 10 is directed to "a vector or plasmid comprising a nucleic acid sequence selected from a) SEQ ID NO:1; b) the complement of SEQ ID NO:1;...e) a portion of SEQ ID NO:1 which is at least 500 nucleotides in length;...i) a nucleic acid that encodes SEQ ID NO:2."

The Lamerdin et al. sequence teach all of the 15000 bases of SEQ ID NO:1.

Lamerdin et al. does not directly teach the use of a plasmid or vector. However, the isolated genomic DNA of GenBank Accession No. AD000864 would have been cloned in a vector of some kind.

Liu et al. teach the Univector plasmid-fusion system which can accommodate large DNA inserts and can shuttle the inserts between various cloning vectors (page 1300, Results and Conclusions).

It would have been obvious to the person of ordinary skill in the art at the time the invention was made to have cloned a large genomic fragment in a cloning vector capable of supporting an insert of a large size.

The person of ordinary skill in the art would have been motivated to make those modifications because genomic research requires shuttling large genomic DNA between various vectors that can support large inserts.

The skilled artisan would have had a reasonable expectation of success combining cloning vectors or plasmids of Short et al. with the nucleic acids of Lamerdin et al. because cloning vectors capable of hosting extremely large genomic DNA inserts have been developed, utilized, and marketed for this purpose.

Therefore the method as taught by Lamerdin et al. in view of Liu et al. would have been *prima facie* obvious over the cloned nucleic acid of the instant application.

Claim 11 is directed to "the isolated nucleic acid sequence is operatively linked to a regulatory sequence."

The teachings of Lamerdin et al. and Liu et al. are described above. In addition to the teachings described above, Liu et al. teach "coding regions of genes could

be placed under the control of regulated promoters" (page 1300, column 1).

The person of ordinary skill in the art, as Liu et al. would have been motivated to make those modifications in order to "explore the consequences of altered regulation...also to produce hybrid proteins with unique properties that could be exploited for genetic or biochemical purposes." (page 1300, column 1).

The skilled artisan would have had a reasonable expectation of success combining expression vectors or plasmids with the nucleic acids of Lamerdin et al. because expression vectors capable of hosting extremely large genomic DNA inserts have been developed, utilized, and marketed for this purpose.

Therefore the vector as taught by Lamerdin et al. and Liu et al. would have been *prima facie* obvious over the method of the instant application.

Claim 12 is directed to "a recombinant host cell comprising the vector or plasmid of claim 11."

The teachings of Lamerdin et al. and Liu et al. are described above. In addition to the teachings described above, Liu et al. teach "Expression of UPS-derived constructs in mammalian cells" (page 1302, figure 2, column 3).

The person of ordinary skill in the art would have been motivated to make those modifications in order to "explore the consequences of altered regulation...also to produce hybrid proteins with unique properties that could be exploited for genetic or biochemical purposes." (page 1300, column 1).

The skilled artisan would have had a reasonable expectation of success generating recombinant host cell comprising expression vectors or plasmids with the

nucleic acids of Lamerdin et al. because recombinant host cells comprising expression vectors have been developed, utilized, and marketed for many years

Therefore the vector as taught by Lamerdin et al. and Liu et al. would have been *prima facie* obvious over the method of the instant application.

Conclusion

No claims are allowed. However, a nucleic acid consisting of SEQ ID NO:1 is clear of the art.

Examiner Contact Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Scott Long** whose telephone number is **571-272-9048**. The examiner can normally be reached on Monday - Friday, 9am - 5pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Dave Nguyen** can be reached on **571-272-0731**. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Q. JANICE LI, M.D.
PRIMARY EXAMINER

Scott Long
Patent Examiner
Art Unit 1633